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51 LysIleLeuLysAspGluThrThrLeuGluSerAsnGlyValAlaIleuAs 67
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260 AAAATTCTCAAGGATGAACCACTTGGAAAGCAAGGAGGTTGCTAGAA 309
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seq_name: gb_est2:BM078237

seq_documentation_block:

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LOCUS      BM078237              685 bp      mRNA      linear      EST 14-NOV-2001
DEFINITION MEST116-H10.T3 ISUM4-TN Zea mays cDNA clone MEST116-H10 3', mRNA
sequence.
ACCESSION  BM078237
VERSION    BM078237.1  GI:16925169
KEYWORDS   EST
SOURCE     Zea mays.
ORGANISM   Zea mays.

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REFERENCE  Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
TITLE      clade; Panicoidae; Andropogoneae; Zea.
JOURNAL    1 (bases 1 to 685)
COMMENT    Qiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
           Unpublished Sequence Tags from B73 Maize Seedlings and Silks
           Unpublished (2001)
           Contact: Patrick S. Schnable
           Schnable Laboratory
           Iowa State University
           G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
           Tel: 515-294-0975
           Fax: 515-294-2299
           Email: schnable@iastate.edu

```

Individual basecall and confidence value were assigned using the phred software.
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
tc). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/lucy/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.

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PCR PRIMERS
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAG)
REVERSE: Reverse PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

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FEATURES
source      1..685
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/cultivar="B73"
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/note="Vector: pT73PAC. Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5'
AAGTGAAGAATTGCGCGCGCAGCAATTTTTTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
BASE COUNT      177 a      169 c      155 g      184 t
ORIGIN

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alignment_scores:
    Quality: 154.00      Length: 154
    Ratio: 1.000        Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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alignment_block:

US-09-805-550-2 x BM078237/rev ..

Align seg 1/1 to reverse of: BM078237 from: 1 to: 685

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248 AlaAsnProLeuAsnLeuPheProGlnGlyValProSergLysSers 264
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684 GCAATTCCTTTGACCTTTTCTCAGGGTGTCCAAAGTGGTGGTCCAA 635
264 nProGlyValAlaProGlyAlaGlySergLysAlaLeuAspAlaLeuArg 281
|||||
634 CCAGGTGTTGTTCCAGTGCGAGGATCGTGCTGTTGATGCTTCCGAC 585
281 InLeuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGln 297
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584 ACCTTCCACAGTTTCAAGCAGCTCTTCACTAGTTCAGGCTAATCCTCA 535
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|||||
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314 uArgLeuIleGlnGlnLeuAsnGlnAlaGluPheLeuArgLeuValAsnGln 331
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484 GCGGTGATTCAGAAATCAAGCTGAGTTCCTCGCTTGGTGAATGAT 435
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348 ValProGlnThrLeuThrValThrProGlnGluArgGluAlaIleGlnAr 364
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364 gLeuGlnGlyMetGlyPheAsnArgGluLeuValLeuGlnValAlaPhePhe 381
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334 GCTCAGGGAATGGGTTCAACCGTGAGCTGTGCTAGAAAGTTTCTTGG 285
381 lacysAsnLysAspGluGluLeuThrAlaAsnTyrLeuLeuAspHisGly 397
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seq_name: gb_est1:AM057042
seq_documentation_block:
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DEFINITION  660008A08.y1 660 - Mixed stages of anther and pollen Zea mays cDNA,
            mRNA sequence.
ACCESSION  AM057042
VERSION    AM057042.1  GI:5932681
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 580)
AUTHORS   Walbot, V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
          University
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 660008 row: A column: 08.

FEATURES
   source          1..580
                   /organism="Zea mays"
                   /cultivar="Ohio43"
                   /db_xref="taxon:4577"
                   /clone_lib="660 - Mixed stages of anther and pollen"
                   /tissue_type="whole premeiotic anthers to pollen shed"
                   /dev_stage="premeiotic anthers to pollen shed"
                   /lab_host="XLOLR"
                   /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI;
                   Site_2: XhoI; anther and pollen cDNA library.
                   directionally sequenced with 5' end at the EcoRI site.
                   Created by Amie Franklin."

BASE COUNT      136 a      160 c      139 g      145 t
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331  GCAGGCGCATCACCCGCTCAGCCAGCATGTTCATTCGCCAGTCAGCCAT 380
240  eProAlaSerAlaGlyProAsnAlaAsnProLeuAsnLeuPheProGln 256
381  CACCTGCCTCTGCAGGGCGCTAATGCAAATCTTGAACCTTTCTCTAG 430
257  GlyValProSerGlyGlySerAsnProGlyValValProGlyAlaGlySe 273
431  GGTCTCCAACTGGGGGTCCACCCAGCTGTGTTCAGGTGAGATC 480
273  rGlyAlaLeuAspAlaLeuArgGlnLeuProGlnPheGlnAlaLeuLeuG 290
481  TGGTCTCTTGATGCTTGCAGACCTTCACAGTTTCACACCTCTTC 530
290  InLeuValGlnAlaAsnProGlnLeuGlnProMetLeu 303
531  AGTTAGTCAGGCTAATCTTCAATCTTCAGCCAAATCTT 571

seq_name: gb_est2:BM337351
seq_documentation_block:
LOCUS      BM337351                700 bp    mRNA    linear    EST 16-JAN-2002
DEFINITION  MEST149-E08.T3 ISUM5-RN Zea mays cDNA clone MEST149-E08 3', mRNA
            sequence.
ACCESSION  BM337351
VERSION    BM337351.1  GI:18167512
KEYWORDS   EST.
SOURCE     Zea mays.
ORGANISM   Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoidae; Andropogoneae; Zea.
            1 (bases 1 to 700)
REFERENCE  Men, T.-J., Oiu, F., Guo, L., Ashlock, D. A and Schnable, P. S.
            Expressed Sequence Tags from B73 Maize: various stages and tissues
            including seedlings treated with a variety of hormones
            Unpublished (2001)
JOURNAL    Schnable Laboratory
            Contact: Patrick S. Schnable
            Iowa State University
            G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
            Tel: 515-294-0975
            Fax: 515-294-2299
            Email: schnable@iastate.edu
            Individual basecall and confidence value were assigned using the
            phred software.
            (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
            it). Overall sequence quality assessment and vector trimming were
            conducted using the Lucy software (<http://www.tigr.org/softlab/>).
            Lucy parameters were set to ensure an overall trimmed quality of
            97.5% or better without any vector fragments in the chosen
            high-quality region of each sequence. Low-quality bases between the
            poly-T and the high-quality region were replaced with N's to serve
            as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES
   source          1..700
                   /organism="Zea mays"
                   /cultivar="B73"
                   /db_xref="taxon:4577"
                   /clone_lib="MEST149-E08"
                   /clone_1ib="ISUM5-RN"
                   /tissue_type="mixed"
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                   /note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
                   Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
                   Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels
                   (3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
                   ), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
                   cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated

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first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACPG (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscissic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGGAAGATTCGGCCGAGCAATTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol- α -catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pRTT3AC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996).

BASE COUNT 181 a 179 c 155 g 185 t
ORIGIN

alignment_scores:
Quality: 144.00 Length: 144
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x BM337351/rev ..
Align seg 1/1 to reverse of: BM337351 from: 1 to: 700

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258 ValProSerGlyGlySerAsnProGlyValValProGlyAlaGlySerG 274
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699 GTTCCAAAGTGGTGGTCCAAACCAAGTGTGTTCCAGGTGAGATCTGG 650
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274 ValAlaLeuAspAlaLeuArgGlnLeuProGlnPheGlnAlaLeuGlnL 291
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649 TCCTCTTGATGGCTTGCAGAGCTTCACAGTTTCAGACACTCTCACT 600
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291 euValGlnAlaAsnProGlnIleLeuGlnPheMetLeuGlnIleuGly 307
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599 TAGTCCAGGCTATCTCAATCTTGCACCAATGCTTCAAGAGCTAAGGT 550
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549 AATCAAAACCCCAATTTCTGGGTTGATTCAGGAAATCAAGCTAGTT 500
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324 eLeuArgLeuValAsnGluSerProGlnGlyProGlyGlyAsnIleL 341
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499 TCTCCGCTTGGTGAATGATCTCTGAGGGTGGTCTGAGGGAACATAC 450
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299 ACTACCTCTTGATCATGCGCATGAGTTTGAC 268

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seq_name: gb_est2:BM380735

seq_documentation_block:

LOCUS BM380735 670 bp mRNA linear EST 16-JAN-2002
DEFINITION MEST524-C09.univ ISUM6 Zea mays cDNA clone MEST524-C09 3', mRNA sequence.
ACCESSION BM380735
VERSION BM380735.1 GI:18179525
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 670)
Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299

REFERENCE

Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones unpublished (2001)

JOURNAL

CONTACT: Patrick S. Schnable
Schnable Laboratory
Iowa State University
405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299

COMMENT

Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the phred software (http://www.phrap.org/). Overall sequence quality assessment and vector trimming was conducted using the Lucy software (version 1.16s, http://www.tigr.org/softlab/). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high quality region of each sequence. Low quality bases between the poly-T and the high quality region were replaced with N's to serve as spacers using a Perl program (est_process.pl), written by Dr. Hui-Hsien Chou.

PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG)
Seq primer: universal (GTA AAA CGA CGG CCA GT)
POLYA=Yes.

FEATURES

source

location/Qualifiers

1..670

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="MEST524-C09"

/clone_1bp="ISUM6"

/tissue_type="mixed"

/lab_host="DH10B"

/note="Vector: pSLiP7 (4.43 kb); Site_1: EcoRI; Site_2: NotI; Tissue samples were collected and partially pooled prior to RNA extraction. First-strand cDNAs were prepared from 21 individual pools of oligo-dT selected mRNAs by priming with 21 different NotI oligo-dT tag primers (5'-AACTGGAAGATTCGGCCGAGCAATTTTCTTTT-3'). Distiguishable 'bar code' tags, (N)6, were used for each separate first-strand cDNA synthesis. Hence, these bar code tags can be used to identify the mRNA pool from which a particular cDNA clone was derived. The 'bar code' tags associated with specific tissue sources are:

ATAGCC--Germinated seeds and seedlings (1, 2, 8, 11 DAG);
ACTGCG--Mixed mature tissues (17, 21, 38, 69, 77 DAG);
CACAGC--Kernels (3, 5, 10, 15, 20, 25, 30, DAP);
TAACCC--Adventitious roots (65 DAG); CAGCGC--Tassels (3-39 cm, 53 and 56 DAG); AGGTAC--Immature ears (0.2-3.0 cm, 53, 56, 59 DAG); TGAGCG--Husks (73 DAG); GACGAC--Silks;
AATCGG--unpollinated first ears; CTAGAG--ear shanks;
GAAGAG--etiolated seedlings; AGTGA--callus;
GTGAGC--Cycloheximide-treated callus; GTGACC--Anaerobic treated seedlings; GATCCA--NAA (a-Naphthalene acetic acid)-treated seedlings; GATGCC--Kinetin-treated seedlings; AAGAC--ACPC (1-aminocyclopropane-1-carboxylic acid)-treated seedlings; GCTCA--Brassinolide-treated seedlings; CTAGCC--ABA (Abscissic acid)-treated seedlings;

TACGGA--GA (Gibberellic acid)-treated seedlings;
GCAGGA--JA (Jasmonic acid)-treated seedlings; Equal
amounts of first-strand cDNA from each reaction were
combined and used as template for DNA Pol-catalyzed 2nd
strand synthesis. After the addition of EcoRI adaptors,
ds-cDNAs were digested with NotI. Molecules between 0.5
and 2.0 kb were directionally cloned into the EcoRI and
NotI sites of the pSLIP1 expression vector. Plasmid DNA
isolated from the library was digested with NotI to remove
empty vector clones. Linear DNAs from 5.4 to 7 kb were gel
purified and ligated at low concentration to promote
recircularization. Ligation products were precipitated and
transformed into DH10B host cells. The complexity of the
resulting library was 1.2 x 10⁶.

BASE COUNT 172 a 170 c 148 g 180 t
ORIGIN

alignment_scores:

Quality: 137.00 Length: 137
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x BM380735/rev ..

Align seg 1/1 to reverse of: BM380735 from: 1 to: 670

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670 CCAGGGTGTGTCAGAGTGCAGGATCTGCTGCTGATCCCTGGCAGCA 621
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281 nleuProGlnPheGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGln1 298
|||||
620 GCCTCCACAGATTCAAGCACTCCTCAGTTAGTCCAGGCTAAATCCTCAA 571
|||||
298 leuGlnProMetLeuGlnGlnLeuGlyLysGlnAsnProGln1leu 314
|||||
570 TCTTGCAGCCCAATGCTTCAAGACCTAGGTAAACCAACCAATTTCTG 521
|||||
315 ArgLeuIleGlnGlnAsnGlnAlaGlnPheLeuArgLeuAlaAsnGln 331
|||||
520 CGGTATATCAGGAATATCAAGCTGAGTTCTCCGCTGGTGAATGATC 471
|||||
331 rProGlnGlyGlyProGlyLysAsnIleLeuGlyGlnLeuAlaAla1av 348
|||||
470 TCCTGAGGGTGTCTCGAGGGAACATACAGTCAATGCGACGTCGTCG 421
|||||
348 a1ProGlnThrLeuThrValThrProGlnGluArgGluAlaIleGlnArg 364
|||||
420 TGCCACAAACGCTGACAGATTACCCAGAGGAAAGGAGGCTATCCAGCG 371
|||||
365 leuGlnGlyMetGlyPheAsnArgGluLeuValLeuGlnValPhePheAl 381
|||||
370 CTCGAGGGAATGGGTTCAACCGTGAAGCTGTCTGAAGATTTTCTTTCG 321
|||||
381 acYAsnIlyAspGluLeuThrAlaAsnTYrLeuLeuAspHisGlyH 398
|||||
320 ATGCAACAAGAGAGAGCTTACAGCAACTACCTCTGATCATATGCC 271
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398 lsgIuPheasp 401
|||||
270 ATGAGTTTTCAC 260

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seq_name: gp_est1:A1947481

seq_documentation_block:

LOCUS A1947481 497 bp mRNA linear EST 19-AUG-1999
DEFINITION 614047B04.x1 614 - root cDNA library from Walbot Lab. Zea mays cDNA,
mRNA sequence.
ACCESSION A1947481
VERSION A1947481.1 GI:5739686
KEYWORDS EST.

SOURCE

Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 497)

Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford
University

Unpublished (1999)

JOURNAL

Contact: Walbot V

Department of Biological Sciences

Stanford University

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Fax: 650 725 8221

Email: walbot@stanford.edu

Plate: 614047 row: B column: 04.

FEATURES

source

1..497

/organism="Zea mays"

/cultivar="W23"

/db_xref="taxon:4577"

/clone_lib="614 - root cDNA library from Walbot Lab"

/tissue_type="root"

/dev_stage="3-4 days old"

/lab_host="X10LR"

/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LW)"

BASE COUNT

117 a 137 c 121 g 121 t

1 others

ORIGIN

alignment_scores:

Quality: 133.00 Length: 133
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x A1947481/rev ..

Align seg 1/1 to reverse of: A1947481 from: 1 to: 497

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269 ProGlyAlaGlySerGlyAlaLeuAspAlaLeuArgGlnLeuProGlnP 285
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484 CCAGGTCTGATGATGCTGCTGATGATGCTGCTGCTGCTGCTGCTGCT 435
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285 eGlnAlaLeuLeuGlnLeuValGlnAlaAsnProGlnIleLeuGlnProm 302
|||||
434 TCAAGCACTCCTCAGTTAGTCCAGGCTAAATCCTCAATCTGCGAGCCAA 385
|||||
302 etLeuGlnGlnLeuGlyLysGlnAsnProGlnIleLeuArgLeuIleGln 318
|||||
384 TGCCTTCAAGAGCTGATTAACCAAAACCCCAAAATTCGCGGTGATTCAG 335
|||||
319 GlnAsnGlnAlaGlnPheLeuArgLeuValAsnGlnSerProGlnIlyG1 335
|||||
334 GAAATATCAAGCTGAGTTTCTCCGCTTGTGATTAATCTCTCGAGGTGG 285
|||||
335 yProGlyLysAsnIleLeuGlyGlnLeuAlaAlaAlaValProGlnThrL 352
|||||
284 TCCTGAGAGGAACATACCTAGTCAATGCGAGCTGCTGCTGCGCCAAAGC 235
|||||
352 eutThrValThrProGlnGluArgGluAlaIleGlnArgLeuGlyMet 368
|||||
234 TGAAGTTACCCAGAGGAACGGAGGCTATCCAGCGGCTCGAGGGAATG 185
|||||
369 G1yPheAsnArgGluLeuValLeuGluValPhePheAlaCysAsnLysAS 385
|||||
184 GGTTCACACCGTGAAGCTTGTGCTGAAGTTTCTTTCGATGACCAAGGA 135
|||||
385 pGluGlnLeuThrAlaAsnTYrLeuLeuAspHisGlyHisGluPheasp 401

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134 CGAAGCTTACGCCACTACCTCTCGATCATGCGCCATGAGTTTGAC 86

seq_name: gb_est1:AW000280
seq_documentation_block:
LOCUS AW000280 565 bp mRNA linear EST 08-SEP-1999
DEFINITION 614010B04.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
mRNA sequence.
ACCESSION AW000280
VERSION AW000280.1 GI:5847201
KEYWORDS EST.
SOURCE ze mays.
ORGANISM Zea mays.
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 565)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 723 8221
Email: walbot@stanford.edu
Plate: 614010 row: B column: 04.
FEATURES
source
1. 565
/organism="Zea mays"
/cultivar="W3"
/db_xref="taxon:4577"
/clone_id="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
Lab (LM)"
BASE COUNT 139 a 133 c 148 g 145 t
ORIGIN
alignment_scores:
Quality: 133.00 Length: 133
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
Alignment_block:
US-09-805-550-2 x AW000280 ..
Align seg 1/1 to: AW000280 from: 1 to: 565
269 ProctylalaglyserglyAlalaenaspAlalaenargInleuProglInph 285
|||||
61 CCAAGTGTGATCTGTGCTTATGCTTGCACAGCTTCACAGTT 110
285 eGlnAlaleuInleuInleuValGlnAlaInleuProglInleuInleuInpro 302
|||||
111 TCAAGCACTCCTTCAGTAGTCAGGCTATATCTCAATCTTGACGCCA 160
302 eLleuGlnGlnleuGlnleuGlnAsnProglInleuArgleuInleuIn 318
|||||
161 TGCTTCAGAGAGCTAGTAACAAACCAACAAATCTCGGTTGATTCAG 210
319 GlnAsnGlnAlaGlnPheleuArgleuValAsnGlnuserProglGlycI 335
|||||
211 GAAATCAAGCTGAGCTTCTCGCTTGGTGAATGAATCCTCGAGAGGTGG 260
335 yProglGlyAlaInleuGlnleuGlnleuAlalaInleuAlaInleuProglInthrl 352

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|||||
261 TCTTGAGGAGAACATPACTAGTCACTGCGAGCTGTGCACAAACGC 310
352 eUthrValThrProglGlnArgleuAlaInleuInleuInleuInleuInmet 368
|||||
311 TGACAGTACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
369 GlnPheAsnArgleuInleuValPhePheAlaCysAsnLysAs 385
|||||
361 GGGTTCACCGTAGCTGTGCTAGAACTTTCTTTCATGCAACAAAGGA 410
385 pGlnGlnleuUthrAlaAsnTyrlleuInleuAspHISGlyHISGlnPheAsp 401
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411 CGAAGCTTACGCCACTACCTCTCGATCATGCGCCATGAGTTTGAC 459

seq_name: gb_est2:BM266651
seq_documentation_block:
LOCUS BM266651 663 bp mRNA linear EST 18-DEC-2001
DEFINITION MEST384-H08.T3 ISUM5-RN Zea mays cDNA clone MEST384-H08 3', mRNA
sequence.
ACCESSION BM266651
VERSION BM266651.1 GI:17929739
KEYWORDS EST.
SOURCE ze mays.
ORGANISM Zea mays.
Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 663)
AUTHORS Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
JOURNAL Unpublished (2001)
COMMENT Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
phred software,
<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rl). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlib/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
FEATURES
source
1. 663
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST384-H08"
/clone_id="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAF), Adventitious roots (95 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cycloheximide-treated callus, Anaerobic treated seedlings
, NAA (a-Naphthalene acetic acid)-treated seedlings,

```

kinetin-treated seedlings, ACPC (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, brassinolide-treated seedlings, ABA (abscisic acid)-treated seedlings, GA (gibberellic acid)-treated seedlings, JA (jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACCTGAGAAATTCGCGCCGACGAGAAATTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcello Bento Soares (genome Research 6: 791-806, 1996).

BASE COUNT 167 a 169 c 147 g 180 t
ORIGIN

alignment_scores:
Quality: 133.00 Length: 133
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x BM26651/rev ..

Align seg 1/1 to reverse of: BM26651 from: 1 to: 663

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662 CAGAGTCAGAGACTGTGCTGTGATGCCCTGGACAGCTTCACAGTT 613
|||||
285 eGlnAlaLeuLeuGlnleuValGlnAlaAsnProGlnleuLeuGlnProm 302
|||||
612 TCAGACCTCTTCAGTTAGTCCAGGCTAACTCCAAATCTTGCAGCCAA 563
|||||
302 etLeuGlnleuLeuGlyGlnAsnProGlnleuLeuArgleuIleGln 318
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562 TGCTTCAGAGCTAGGTAACCAAAACCAAAATTCGCGTTGATTCAG 513
|||||
319 GlnAsnGlnAlaGlnPheLeuArgleuValAsnGlnSerProGlnGly 335
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512 GAAATCAAGCTGAGTTTCGCGTTGGTGAATGATCTCTGAGGGTGG 463
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335 yProGlyGlyAsnIleLeuGlyGlnleuAlaAlaValProGlnThrL 352
|||||
462 TCCTGGAGGGAACATAGTCAACTGCGAGCTGTGCGCAAAACGC 413
|||||
352 euthrValThrProGlnGlnArgGlnAlaIleGlnArgleuGlnGlyMet 368
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412 TGACAGTACCCAGAGAAACGGAGGCTATCCAGGCTCGAGGGAATG 363
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369 GlyPheAsnArgGlnleuValleuGlnValPhePheAlaCysAsnLys 385
|||||
362 GGGTTCAACCGTGAGCTTGCTGAGAGTTTCTTTCGATGCCAACAGA 313
|||||
385 pGlnGlnleuThrAlaAsnTyrlleuLeuAspHisGlyHisGlnPheAsp 401
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312 CGAAGACCTTACAGCCAACTCCGATCATGAGCCATGAGTTTGAC 264
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seq_name: gb_est1:A1759136

seq_documentation_block:

LOCUS A1759136 530 bp mRNA linear EST 02-FEB-2000
DEFINITION 605085E11.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
CDNA, mRNA sequence.
ACCESSION A1759136
VERSION A1759136.1 GI:5152838
KEYWORDS EST.

SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 530)
AUTHORS Walbot,V.
TITLE Malze ESTs from various cDNA libraries sequenced at Stanford
UNIVERSITY
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 605085 row: E column: 11.
Location/Qualifiers
1..530
/organism="Zea mays"
/cultivar="Oh1043"
/db_xref="taxon:4577"
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/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
/note="Organ: Kernel; Vector: pMD-GAL4-2'; Site_1: EcoRI;
Site_2: XhoI; Kernel endosperm cDNA library from Schmidt
lab"

FEATURES
source

BASE COUNT 137 a 135 c 121 g 137 t
ORIGIN

alignment_scores:
Quality: 117.00 Length: 117
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-805-550-2 x A1759136/rev ..

Align seg 1/1 to reverse of: A1759136 from: 1 to: 530

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529 TTTCAAGCAGCTCTTCACTTACTCCAGGCTAATCTCAAAATCTTGACGC 480
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301 oMetLeuGlnleuLeuGlyGlnAsnProGlnleuLeuArgleuIleG 318
|||||
479 AATGCTTCAGAGCTAGGTAACCAAAACCCCAAAATTCGCGGTGATTC 430
|||||
318 lnglAsnGlnAlaGlnPheLeuArgleuValAsnGlnSerProGlnGly 334
|||||
429 AGGAAATCAAGCTGAGTTTCTCCGCTTGGAAGAATCTCTGAGGGT 380
|||||
335 GlyProGlyGlyAsnIleLeuGlyGlnleuAlaAlaValProGlnThr 351
|||||
379 GCTCTGAGAGGAACATAGTCAACTGCGAGCTGTGCGCAAAAC 330
|||||
351 rLeuThrValThrProGlnGlnArgGlnAlaIleGlnArgleuGlnGlyM 368
|||||
329 GCTGACAGTACCCAGAGAAACGGAGGCTATCCAGGCGCTCGAGGGA 280
|||||
368 etGlyPheAsnArgGlnleuValleuGlnValPhePheAlaCysAsnLys 384
|||||
279 TGGGTTCAACCGTGAGCTTGCTGAGAGTTTCTTTCGATGCCAACAG 230
|||||
385 AspGlnGlnleuThrAlaAsnTyrlleuLeuAspHisGlyHisGlnPheAs 401
|||||
229 GACGAGAGCTTACAGCCAACTACTCTCTGATCATGCGCATGAGTTTGA 180
|||||
```

401 p 401

Brassinolide-treated seedlings, ABA (Abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' ACTGGAGAGATTCGGCCGACGAGAAATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

BASE COUNT 147 a 151 c 124 g 166 t

ORIGIN

alignment_scores:

Quality: 106.00 Length: 106
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x BM075107/rev ..

Align seg 1/1 to reverse of: BM075107 from: 1 to: 588

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296 ProGlnIleuGlnProMetIleuGlnIleuGlyLysGlnAsnProG1 312
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587 CCTCAATCTTCAGGCAATGCTTCAAGAGCTAGTAAACAAACCCACA 538
312 nIleuArGleuIleGlnIleuAsnIleuIleuValIleuValIleuVal 329
|||||
537 AATTCTCGGCTGATTCAAGAAATCAAGCTGAGTTCTCGCTGGTGA 488
329 snGluSerProGluGlyGlyProGlyGlyAsnIleuGlyGlnIleuAla 345
|||||
487 ATGAATCTCTGAGGGTGTCTCGAGGAGACATAGTCAACGCGCA 438
346 AlaIleuValProGlnThrIleuThrValIleuProGluGlnIleuAla 362
|||||
437 GCTGCTGCTCCACAAACGCTGACAGTACCACAGAGAGGAGGCTAT 388
362 eGlnArGleuGluGlyMetGlyPheAsnArGluIleuValIleuValIleuVal 379
|||||
387 CCAGCGGCTCGAGGAGATGGGTTCAACGCTGAGCTTGCTAGAAATT 338
337 TCTTTGCAATGCAACAGAGAGAGAGCTTACAGCCAACTACCTCGTGAT 288
379 hepPheIleuGlyAsnIleuGlyGlnIleuValIleuValIleuValIleuVal 395
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337 TCTTTGCAATGCAACAGAGAGAGAGCTTACAGCCAACTACCTCGTGAT 288
396 HisGlyHisGluPheAsp 401
|||||
287 CATGGCCATGAGTTTGAC 270

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seq_name: gb_est1:AI783295

seq_documentation_block:

LOCUS AI783295 382 bp mRNA linear EST 01-JUL-1999
DEFINITION 614010B04.x2 614 - root cDNA library from Walbot Lab Zea mays cDNA,
mRNA sequence.

ACCESSION AI783295
VERSION AI783295.1 GI:5325104

KEYWORDS EST.
SOURCE Zea mays.

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 382)

AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614010 row: B column: 04.
Location/Qualifiers

FEATURES

source

1..382

/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLOLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site: 1:
EcoRI; Site: 2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
Lab (LM) 92 a 97 c 101 g 92 t

BASE COUNT 92 a 97 c 101 g 92 t

ORIGIN

alignment_scores:

Quality: 105.00 Length: 105
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-805-550-2 x AI783295 ..

Align seg 1/1 to: AI783295 from: 1 to: 382

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269 ProGlyValGlySerGlyAlaIleuAspAlaIleuArgIleuProGlnP 285
|||||
68 CCAGGTCTGATCTGGTGGCTTGATGCTTGCGACAGCTTCACAGTT 117
285 eGlnAlaIleuGlnIleuValGlnAlaAsnProGlnIleuGlnIleuGln 302
|||||
118 TCAAGCACCTCTTCACTAGTACGAGCTATTCCTCAATCTTCGAGCA 167
302 etleuGlnIleuGlyGlyGlnAsnProGlnIleuArgIleuIleuGln 318
|||||
168 TGCTTCAAGAGCTAGTAAACAAACCCAAATTCGCGTTGATTGAG 217
319 GluAsnGlnIleuGlnPheIleuArgIleuValAsnGluSerProGluGly 335
|||||
218 GAAATCAACCTGAGTTCTCCGCTTGCTGAATGAATCTCTGAGGTGG 267
335 yProGlyGlyAsnIleuGlyGlnIleuAlaIleuValProGlnThrL 352
|||||
268 TCTTGAGAGGAAACATAGTCAACTGCAGCTGCTGCCACAAACGC 317
352 eurThrValIleuProGluGlnIleuValIleuGlnIleuGlnIleuGln 368
|||||
318 TGACAGTTACCCCGAGAGAGGAGGCTATCCAGCGGCTCGAGGAGATG 367
369 GlyPheAsnArGlu 373
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368 GGGTTCAACCGTGA 382

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seq_name: gb_est2:BI991866

seq_documentation_block:

LOCUS BI991866 609 bp mRNA linear EST 24-OCT-2001
DEFINITION 1020052G08.x1 1020 - unigene II from Maize Genome Project Zea mays
cDNA, mRNA sequence.

ACCESSION BI991866

VERSION	BI991866.1	GI:16377325
KEYWORDS	EST.	
SOURCE	Zea mays.	
ORGANISM	Zea mays	
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade: Panicoideae; Andropogoneae; Zea.	
AUTHORS	Walbot,V	
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 1020052 row: G column: 08.	
FEATURES	Location/Qualifiers	
source	1..609 /organism="Zea mays" /db_xref="taxon:4577" /clone_lib="1020 - Unigene II from Maize Genome Project" /note="this library represents the unique genes found in the second round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 947 and 949. Contigs were assembled using zmbassembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."	
BASE COUNT	168 a	158 c 129 g 154 t
ORIGIN		
alignment_scores:		
Quality:	104.00	Length: 104
Ratio:	1.000	Gaps: 0
Percent Similarity:	100.000	Percent Identity: 100.000
alignment_block:		
US-09-805-550-2 x BI991866/rev	..	
Align seg 1/1 to reverse of: BI991866 from: 1 to: 609		
298	IleleugInPromeLleugInGuLeuGInLySgInAsPProGInIlele 314	
609	ATCTTCAGCCAAATGCTTCAAGACGTGATTAAGCAAAACCCCAATTC 560	
314	uArgLeuIleGInLuSngInAlaGuPheLeuAqGLeuValAsnGluS 331	
559	GCGGTGATTTCAGGAAATCAAGCTGAGTTCTCCGGTGGTGAAGAA 510	
331	ePProGInGuLyG1PProG1yG1yAsnIleLeuGInGuIneAlaAla 347	
509	CTCTGAGGGGTGCTCGAGGAGACCTACTAGTCACTGGAGCTGCT 460	
348	ValPProGInThrLeuThrValThrProGInGu1uAqS1uAlaIleGIn 364	
459	GTGCCACAAACGTCGACGTTACCCGACGAGAAACGGAGGCTATCCAGC 410	
364	GLeuGInGuLyMeC1yPheAsnAqG1uLeuValLeuG1uValPhePhea 381	
409	GCTCGAGGGAATGGGGTTCAACCGTGAGCTTGCTAGAAAGTTCTTGG 360	
381	IaCyAsnLyAspG1uLeuThrAlaSnLyTrLeuLeuAspHISG1y 397	
359	CATGCAACAAAGACGAAGCTTACACCAACCTACCTCCGATCATGGC 310	
398	HISg1uPheAsp 401	
309	CATGAGTTTGAC 298	

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seq_name: gb_est1:AW155658
seq_documentation block:
LOCUS      AW155658          589 bp      mRNA      linear      EST 04-NOV-1996
DEFINITION 614097/D1.1 y1 614 - root cDNA library from Walbot Lab Zea mays cDNA.
ACCESSION  mRNA sequence.
VERSION    AW155658
KEYWORDS   AW155658.1 GI:6227129
SOURCE     EST.
ORGANISM   Zea mays.
            Zea mays
            Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 589)
REFERENCE  Walbot, V.
            Maize ESTs from various cDNA libraries sequenced at Stanford
            University
            Unpublished (1999)
JOURNAL    Contact: Walbot V
COMMENT    Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 614097 row: D column: 11.
FEATURES   Location/Qualifiers
            source          1..589
                        /organism="Zea mays"
                        /cultivar="W23"
                        /db_xref="taxon:4577"
                        /clone_lib="614 - root cDNA library from Walbot Lab"
                        /tissue_type="root"
                        /dev_stage="3-4 days old"
                        /lab_host="X10LR"
                        /note="Organ: root; Vector: pBluescriptII SK+; Site_1:
                        EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot
                        Lab (LM)"
BASE COUNT  139 a      169 c      139 g      140 t      2 others
ORIGIN
alignment_scores:
            Quality: 100.00      Length: 100
            Ratio: 1.000      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
US-09-805-550-2 x AW155658      ..
Align seg 1/1 to: AW155658 from: 1 to: 589
160  LeuGIuGInThrIleGInGlnIleLeuAspMetGlyGlyGlyThrTrpEl 176
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168  CTAGACACACATCATCCACMAATTCCTTGACATGGGTGGTGCATCGGGA 217
|||||
176  uATGAsPThrValValArgAlaLeuArgAlaIaIaTyRAsnAsnProGluA 193
|||||
218  ACGTATACAGTTGTCGTCGCTCTACGCTCGCATACATACACCCTGACA 267
|||||
193  tGAlaIaIleAsPtyrLeuTyRserGlyIleProGluAsnValGluAlaGln 209
|||||
268  GAGCTATAGACTACCGTATTCGTGAATTCGAGAAATCGAGAAATCGAGCCTG 317
|||||
210  ProValAlaIaArgAlaProAlaAlaGlyGlnGlnIThrAsnGlnAlaAla 226
|||||
318  CCTGTTGCCCGAGCACCTGCTCTGCGCAACAACAAATCAGCAGGCCGC 367
|||||
226  AserProAlaGlnProAlaValAlaLeuProValGlnProserProAlaS 243
|||||
368  ATCACCCTCGCTCAGCAGCAGTTGCATGTGCATGCGCCTATCACCTGCTT 417

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243 ealAaGlyProAsnAlaAsnProLeuAsnLeuPheProGlnGlyValPro 259
|||||
418 CTGCAGGCGCTTAATGCAAAATCCTTTGAACCTTTCTCCTCAGGCTGTCCA 467
seq_name: gb_est1:AI834654

seq_documentation_block:
LOCUS      AI834654                495 bp      mRNA      linear      EST 02-FEB-2000
DEFINITION 606071D12.x1 606 - Ear tissue cDNA library from Schmidt lab Zea
mays cDNA, mRNA sequence.
ACCESSION  AI834654
VERSION    AI834654.1  GI:5468863
KEYWORDS   EST.
SOURCE     Zea mays.
            Zea mays.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 495)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
          University
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 606071 row: D column: 12.
FEATURES
source
1..495
   /organism="Zea mays"
   /cultivar="Ohio43"
   /db_xref="taxon:4577"
   /clone_lib="606 - Ear tissue cDNA library from Schmidt
   lab"
   /tissue_type="mixed"
   /dev_stage="ear length from 0.5 cm - 2.0 cm"
   /lab_host="XLOLR (Stratagene)"
   /note="Organ: Immature ear; Vector: pBK-CMV; Site_1: EcoRI
   ; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt
   lab"
BASE COUNT  125 a      129 c      103 g      138 t
ORIGIN
alignment_scores:
  Quality:      89.00      Length:      89
  Ratio:        1.000      Gaps:        0
  Percent Similarity: 100.000  Percent Identity: 100.000
alignment_block:
US-09-805-550-2 x AI834654/rev ..
Align seg 1/1 to reverse of: AI834654 from: 1 to: 495
313 lleuAArgleuIleGlnGluAnGlnAlaGluPheLeuArgLeuValAs 329
|||||
494 ATTCTGCGGTGATTCAGAAAATCAAGCTGAGTTCTCGCTGTGAGAA 445
329 ngIuSerProGluGlyGlyProGlyGlyAsnIleLeuGlnIleuAlaA 346
|||||
444 TGAATCTCTGAGGCTGCTCTGAGGGAACATACCTAGCTCACTGGCAG 395
346 laAlaValProGlnThrLeuThrValThrProGluGluArgGluAlaIle 362
|||||
394 CTGCTGTGCCACAACGCTGACAGTTACCCAGAGAACGAGGAGGTATC 345
363 GlnArgLeuGlnGlyMetGlyPheAsnArgGluLeuValLeuGluValPh 379
|||||
344 CAGCGCTCGAGGAGATGGGCTTACCGCTGAGCTTGTCTAGAGTTT 295
379 ePheAlaCysAsnLysAspGluGluLeuThrAlaAsnTyrLeuLeuAspH 396
|||||
294 CTTTGCAATGCACAAGAGCGAAGAGCTTACAGCCACTACTCTCTGATC 245
396 tsGlyHlsGluPheAsp 401
|||||
244 ATGGCCATGAGTTTGAC 228

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